

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 06:56:21 ; Search time 96.4051 Seconds
(without alignments)
1349.183 Million cell updates/sec

Title: US-09-939-537-33

Perfect score: 1385

Sequence: 1 EFKSODKHTCPPCAPBL.....DETCAMAGQGLDGLWTTDP 254

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1356 | 97.9 | 544 | 2 | Q6P395 |
| 2 | 1255 | 91.3 | 509 | 2 | Q8NF17 |
| 3 | 1258 | 90.8 | 330 | 1 | GCI_HUMAN |
| 4 | 1258 | 90.8 | 465 | 2 | Q6GMX6 |
| 5 | 1258 | 90.8 | 466 | 2 | Q6IN78 |
| 6 | 1258 | 90.8 | 469 | 2 | Q727P5 |
| 7 | 1258 | 90.8 | 470 | 2 | Q6PJ44 |
| 8 | 1258 | 90.8 | 470 | 2 | Q725W1 |
| 9 | 1258 | 90.8 | 472 | 2 | Q6N089 |
| 10 | 1258 | 90.8 | 475 | 2 | Q6GMW7 |
| 11 | 1258 | 90.8 | 476 | 2 | Q6GMX1 |
| 12 | 1258 | 90.8 | 679 | 2 | Q96P08 |
| 13 | 1254 | 90.5 | 473 | 2 | Q6P055 |
| 14 | 1254 | 90.5 | 475 | 2 | Q6WZ06 |
| 15 | 1254 | 90.5 | 480 | 2 | Q6N094 |
| 16 | 1254 | 90.5 | 481 | 2 | Q6N097 |
| 17 | 1254 | 90.5 | 482 | 2 | Q72351 |
| 18 | 1252 | 90.4 | 348 | 2 | Q6PYX1 |
| 19 | 1252 | 90.4 | 473 | 2 | Q6MWV7 |
| 20 | 1252 | 90.4 | 478 | 2 | Q6P181 |
| 21 | 1252 | 90.4 | 480 | 2 | Q6P181 |
| 22 | 1251 | 90.3 | 466 | 2 | Q6N096 |
| 23 | 1247 | 90.0 | 475 | 2 | Q6N095 |
| 24 | 1239 | 88.7 | 487 | 2 | Q652L2 |
| 25 | 1171 | 84.5 | 354 | 2 | Q86TT2 |
| 26 | 1171 | 84.5 | 358 | 2 | Q6N030 |
| 27 | 1167 | 84.3 | 521 | 2 | Q8NAY9 |
| 28 | 1151 | 83.1 | 326 | 1 | GC3_HUMAN |
| 29 | 1140 | 82.3 | 417 | 2 | Q6N093 |
| 30 | 1140 | 82.3 | 417 | 2 | Q6N093 |
| 31 | 1137 | 82.1 | 464 | 2 | Q6WZ06 |

| | | | | | | |
|----|-------|------|-----|---|------------|---------------------|
| 32 | 1135 | 81.9 | 465 | 2 | Q6P6C4 | Q6P6C4 homo sapien |
| 33 | 1130 | 81.6 | 327 | 1 | GC4_HUMAN | P01861 homo sapien |
| 34 | 1130 | 81.6 | 473 | 2 | Q8TC63 | Q8TC63 homo sapien |
| 35 | 1126 | 81.3 | 493 | 2 | Q6GCN4 | Q6GCN4 homo sapien |
| 36 | 1121 | 80.9 | 476 | 2 | Q6MZX7 | Q6MZX7 homo sapien |
| 37 | 938.5 | 67.8 | 303 | 2 | Q6KAM2 | Q6KAM2 mus musculi |
| 38 | 938.5 | 67.8 | 398 | 1 | GC3M_MOUSE | P03987 mus musculi |
| 39 | 931.5 | 67.3 | 393 | 1 | GC1M_MOUSE | P01869 mus musculi |
| 40 | 916 | 66.1 | 323 | 1 | GC_RABIT | P01870 oryctolagus |
| 41 | 910.5 | 65.7 | 337 | 2 | Q95M34 | Q95M34 equus caball |
| 42 | 905 | 65.3 | 399 | 1 | GCAM_MOUSE | P01865 mus musculi |
| 43 | 896 | 64.7 | 329 | 1 | GC2_CAVO | P01862 cavia porce |
| 44 | 870.5 | 62.9 | 405 | 1 | GCEN_MOUSE | P01867 mus musculi |
| 45 | 840.5 | 60.7 | 329 | 1 | GC3_MOUSE | P22436 mus musculi |

ALIGNMENTS

RESULT 1
ID Q6P395 PRELIMINARY; PRT; 544 AA.
AC Q6P395;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SOURCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavani T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019046; AAH19046.1; -;
DR HSSP; P01861; IADO.
DR InterPro; IPR003559; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003557; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-se; 3.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IG_C1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

KW Hypothetical protein.
 SQ SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;
 Query Match 97.9%; Score 1356; DB 2; Length 544;
 Best Local Similarity 98.8%; Pred. No. 1,1e-97;
 Matches 249; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVYTCVVVDVSHEDPEVKF 60
 DB 244 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVYTCVVVDVSHEDPEVKF 303
 QY 61 NMVVDGVEVNAKTPREBOYNSTRVSVLTVLHODMLNGEKYCKVSNKALPAPIEKT 120
 DB 304 NMVVDGVEVNAKTPREBOYNSTRVSVLTVLHODMLNGEKYCKVSNKALPAPIEKT 363
 QY 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 180
 DB 364 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 423
 QY 181 PVLDSGSEFLYSKLTVDKSRWQQGNVFCSVVMEALHNHYTQKSLSFGLDPTCAE 240
 DB 424 PVLDSGSEFLYSKLTVDKSRWQQGNVFCSVVMEALHNHYTQKSLSFGLDPTCAE 483
 QY 241 AODGELDGLMTT 252
 DB 484 AODGELDGLMTT 495
 RESULT 2
 ID Q8NF17 PRELIMINARY; PRT; 509 AA.
 AC Q8NF17;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 GN P1J00395 Protein (Fragment).
 GN Name=P1J00395;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.,
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK090464; BAC03445.1; -
 DR PIR; A45874; A45874.
 DR HSSP; P01842; 7PAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF07654; C1-Bet; 3.
 DR SMART; SM00407; IGG1; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 FT NON TER 1
 SQ SEQUENCE 509 AA; 56110 MW; 089498D8076B863C CRC64;
 Query Match 91.3%; Score 1265; DB 2; Length 509;
 Best Local Similarity 91.7%; Pred. No. 1,3e-90;
 Matches 231; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
 QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVYTCVVVDVSHEDPEVKF 60
 DB 209 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVYTCVVVDVSHEDPEVKF 268
 QY 61 NMVVDGVEVNAKTPREBOYNSTRVSVLTVLHODMLNGEKYCKVSNKALPAPIEKT 120
 DB 269 NMVVDGVEVNAKTPREBOYNSTRVSVLTVLHODMLNGEKYCKVSNKALPAPIEKT 328
 QY 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 180
 DB 328 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 387

DB 329 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 388
 QY 181 PVLDSGSEFLYSKLTVDKSRWQQGNVFCSVVMEALHNHYTQKSLSFGLDPTCAE 240
 DB 389 PVLDSGSEFLYSKLTVDKSRWQQGNVFCSVVMEALHNHYTQKSLSFGLDPTCAE 448
 QY 241 AODGELDGLMTT 252
 DB 449 AODGELDGLMTT 460
 RESULT 3
 ID GCI_HUMAN STANDARD; PRT; 330 AA.
 AC P01857;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig gamma-1 chain C region.
 GN Name=IGHG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=82274238; PubMed=6287432;
 RA Ellison J.W., Berson B.J., Hood L.E.;
 RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
 RL Nucleic Acids Res. 10:4071-4079 (1982).
 RN [2]
 RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
 RA MEDLINE=71064024; PubMed=5489771;
 RA Cunningham B.A., Rutishauser U., Gail W.E., Gottlieb P.D.,
 RA Waxdal M.J., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
 RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
 RL Biochemistry 9:3161-3170 (1970).
 RN [3]
 RP SEQUENCE OF 136-329 (EU).
 RA MEDLINE=71064025; PubMed=5530842;
 RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
 RA Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
 RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
 RL Biochemistry 9:3171-3181 (1970).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN NIE).
 RA MEDLINE=77070269; PubMed=826475;
 RA Ponstingl H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
 RT peptides of the H-chain, alignment of the tryptic peptides and
 RT discussion of the complete structure.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).
 RN [5]
 RP SEQUENCE (MYELOMA PROTEIN KOL) AND DISULFIDE BONDS.
 RA MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RN Hoppe-Seyler's Z. Physiol. Chem. 364:713-747 (1983).
 RN [6]
 RP DISULFIDE BONDS.
 RA MEDLINE=71064027; PubMed=4923144;
 RA Gail W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196 (1970).
 RN [7]
 RP DISULFIDE BONDS.
 RA MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges";
RL Hoppe-Seyster's Z. Physiol. Chem. 357:1515-1540 (1976).
RN (8)
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370 (1981).
CC -1- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
CC G1M(1) marker, 239-D and 241-L. KOL and EU sequences have the
CC G1M(3) marker and the G1M (non-1) markers.
CC MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC 116, 198, 269 and 272.
CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC -1- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, J00238; AAC82527.1; ALT_INIT.
DR PIR, A93433; GHNU.
DR PDB, 1A07; X-ray; H=1-103.
DR PDB, 1D5B; X-ray; B/H=1-101.
DR PDB, 1D51; X-ray; H=1-101.
DR PDB, 1D6V; X-ray; H=1-101.
DR PDB, 1DN2; X-ray; A/B=120-326.
DR PDB, 1EAK; X-ray; A/B=106-329.
DR PDB, 1FC1; X-ray; A/B=106-329.
DR PDB, 1FC2; X-ray; D=106-329.
DR PDB, 1FCC; X-ray; A=121-326.
DR PDB, 1H2H; X-ray; H/K=1-330.
DR PDB, 117Z; X-ray; B/D=1-103.
DR PDB, 11TS; X-ray; A/B=107-330.
DR PDB, 11TX; X-ray; A/B=107-330.
DR PDB, 1L6X; X-ray; A=120-326.
DR PDB, 1QOX; X-ray; A/B=119-330.
DR PDB, 2RCS; X-ray; H=1-103.
DR Genew; HGNC:5525; IGHG1.
DR MIM; 147100; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00477; Ig_3.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
DR 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain.
KV
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 Hinge.
FT DOMAIN 111 223 CH2.
FT DOMAIN 224 330 CH3.
FT DISULFID 27 83
FT DISULFID 103 103 Interchain (with light chain).
FT DISULFID 109 109 Interchain (with heavy chain).
FT DISULFID 112 112 Interchain (with heavy chain).
FT DISULFID 144 204
FT DISULFID 250 308

FT CARBOHYD 180 180 N-linked (GlcNAc...).
FT VARIANT 97 97 K -> R (in G1M(3) marker).
FT VARIANT 239 239 /FTid=VAR_003886.
FT VARIANT 241 241 D -> E (in G1M(non-1) marker).
FT VARIANT 241 241 /FTid=VAR_003887.
FT VARIANT 241 241 L -> M (in G1M(non-1) marker).
FT VARIANT 241 241 /FTid=VAR_003888.
FT STRAND 23 24
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FT STRAND 59 61
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FT STRAND 302 303
FT STRAND 306 311
FT STRAND 313 314
FT STRAND 316 318
FT STRAND 319 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EB106C2FA33D CRC64;
Query Match 90.8%; Score 1258; DB 1; Length 330;
Best Local Similarity 100.0%; Pred.No. 2.7e-90;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPKSCDKHTTCCPPAPAEELGGPSVFLPPPKKDTLMTSRTPENVCVVVDVSHEDPEVKF 60
DB 99 EPKSCDKHTTCCPPAPAEELGGPSVFLPPPKKDTLMTSRTPENVCVVVDVSHEDPEVKF 158
QY 61 NMVYDGVETHNAKTPREEQYNSTYRVSVLTTLHODMNLNGEKYCKSNKALPAPIEKT 120
DB 159 NMVYDGVETHNAKTPREEQYNSTYRVSVLTTLHODMNLNGEKYCKSNKALPAPIEKT 218
QY 121 ISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPP 180
DB 219 ISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPP 278

QY 181 PVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVWHEALNHNHYOKSLISLSPG 231
 Db 279 PVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVWHEALNHNHYOKSLISLSPG 329

RESULT 4

OG6MX6 PRELIMINARY; PRT; 465 AA.

AC OG6MX6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI TaxID=9606;
 [1] _TaxID=9606;

SEQUENCE FROM N.A.

RA TISSUE=Primary B-Cells;
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN SEQUENCE FROM N.A.
 RP TISSUE=Primary B-Cells;
 RC Straubeberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC073766; AAH73766.1; --
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig C1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig V.
 DR Pfam: PF07654; C1-set; 3.
 DR SMART: SM00407; Ig; 4.
 DR SMART: SM00409; Ig; 2.
 DR SMART: SM00407; Ig; 1.
 DR PROSITE: PS00835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN 2.
 DR Hypothetical protein
 SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FD81386E CRC64;

Query Match
 Best Local Similarity 90.8%; Score 1258; DB 2; Length 465;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHICPCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 Db 234 EPKSCDKTHICPCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 293
 QY 61 NMYVDGEVHNAKTRPREBOYNSTYRVSVLTITLHODMNGEKYCKSNALKALPAPIEKT 120
 |||

Db 294 NMYVDGEVHNAKTRPREBOYNSTYRVSVLTITLHODMNGEKYCKSNALKALPAPIEKT 353

QY 121 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNGOENNYKTP 353

Db 354 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNGOENNYKTP 180

QY 181 PVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVWHEALNHNHYOKSLISLSPG 231

Db 414 PVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVWHEALNHNHYOKSLISLSPG 464

RESULT 5

OG6IN78 PRELIMINARY; PRT; 466 AA.

AC OG6IN78;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI TaxID=9606;
 [1] _TaxID=9606;

SEQUENCE FROM N.A.

RA TISSUE=Peripheral Nervous System;
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carinanci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN SEQUENCE FROM N.A.
 RP TISSUE=Peripheral Nervous System;
 RC Straubeberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC072419; AAH72419.1; --
 DR HSPB; P01861; IAD0.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig C1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig V.
 DR Pfam: PF07654; C1-set; 3.
 DR SMART: SM00409; Ig; 2.
 DR SMART: SM00407; Ig; 1.
 DR PROSITE: PS00835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN 2.
 SQ SEQUENCE 466 AA; 50853 MW; 53E0BCED81076E CRC64;

Query Match
 Best Local Similarity 90.8%; Score 1258; DB 2; Length 466;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHICPCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
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Db 235 EPKSCDKHTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 294
Qy 61 NMYVDGEVHNATKTKREEQYNSTYRVSVLTLYLHODMLNGKSKYCKKCVSNKALPAPIEKT 120
Db 295 NMYVDGEVHNATKTKREEQYNSTYRVSVLTLYLHODMLNGKSKYCKKCVSNKALPAPIEKT 354
Qy 121 ISAKGQPREPPVYTLPSPRDELTKNOVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTP 180
Db 355 ISAKGQPREPPVYTLPSPRDELTKNOVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTP 414
Qy 181 PVLSDSGSFYLSKLTVDKSRMQGNVFCSVWHEALHNHYTQKSLSLSPG 231
Db 415 PVLSDSGSFYLSKLTVDKSRMQGNVFCSVWHEALHNHYTQKSLSLSPG 465

RESULT 6
Q727P5 PRELIMINARY; PRT; 469 AA.
ID 0727P5;
AC 0727P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sp1leen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Sp1leen;
RA Strausberg R.;
RA Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC051328; AAH51328.1; -.
DR HSSP; P01857; 1HZH.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-sec; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SO SEQUENCE 469 AA; 51395 MW; C0D5B12BAAF795C CRC64;

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Qy 1 EPKSCDKHTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 238 EPKSCDKHTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 297
Qy 61 NMYVDGEVHNATKTKREEQYNSTYRVSVLTLYLHODMLNGKSKYCKKCVSNKALPAPIEKT 120
Db 298 NMYVDGEVHNATKTKREEQYNSTYRVSVLTLYLHODMLNGKSKYCKKCVSNKALPAPIEKT 357
Qy 121 ISAKGQPREPPVYTLPSPRDELTKNOVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTP 180
Db 358 ISAKGQPREPPVYTLPSPRDELTKNOVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTP 417
Qy 181 PVLSDSGSFYLSKLTVDKSRMQGNVFCSVWHEALHNHYTQKSLSLSPG 231
Db 418 PVLSDSGSFYLSKLTVDKSRMQGNVFCSVWHEALHNHYTQKSLSLSPG 468

RESULT 7
Q6RJA4 PRELIMINARY; PRT; 470 AA.
ID 06RJA4;
AC 06RJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-sec; 3.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR Hypothetical protein.
SO SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

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Query Match 90.8%; Score 1258; DB 2; Length 470;
 Best Local Similarity 100.0%; Pred. No. 4.2e-90;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 239 EPKSCDKHTHTCPPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
 QY 61 NMVYDGVAVNNAKTKPREEQYNSTYRVVSVLTVTHQDWLNAGEYKCKVSNKALPAPIEKT 120
 DB 299 NMVYDGVAVNNAKTKPREEQYNSTYRVVSVLTVTHQDWLNAGEYKCKVSNKALPAPIEKT 358
 QY 121 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNNGQPENNYKTTP 180
 DB 359 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNNGQPENNYKTTP 418
 QY 181 PVLDSGSEFLYSKLTVDKSRWQGNNVSCSVMEHALHNYTQKSLSLSPG 231
 DB 419 PVLDSGSEFLYSKLTVDKSRWQGNNVSCSVMEHALHNYTQKSLSLSPG 469

RESULT 8
 Q7ZSW1 PRELIMINARY; PRT; 470 AA.

ID Q7ZSW1
 AC Q7ZSW1;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 GN NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schlier G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Diatchenko L., Marsina K., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Cassavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lodiellano N.A., Peters G.J., Abramson R.D., Mollaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Roditigues S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzanski M.I., Skalka U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RU Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC053984; AAH53984.1; -.
 DR HSSP: P01857; 1HZH.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_c1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF07654; Cl-set; 3.
 DR SMART: SM00406; IGV; 1.
 DR SMART: SM00407; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.

KW Hypothetical protein.
 SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483B1A CRC64;
 Query Match 90.8%; Score 1258; DB 2; Length 470;
 Best Local Similarity 100.0%; Pred. No. 4.2e-90;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 239 EPKSCDKHTHTCPPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
 QY 61 NMVYDGVAVNNAKTKPREEQYNSTYRVVSVLTVTHQDWLNAGEYKCKVSNKALPAPIEKT 120
 DB 299 NMVYDGVAVNNAKTKPREEQYNSTYRVVSVLTVTHQDWLNAGEYKCKVSNKALPAPIEKT 358
 QY 121 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNNGQPENNYKTTP 180
 DB 359 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNNGQPENNYKTTP 418
 QY 181 PVLDSGSEFLYSKLTVDKSRWQGNNVSCSVMEHALHNYTQKSLSLSPG 231
 DB 419 PVLDSGSEFLYSKLTVDKSRWQGNNVSCSVMEHALHNYTQKSLSLSPG 469

RESULT 9

ID Q6N089 PRELIMINARY; PRT; 472 AA.

Q6N089
 AC Q6N089;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686P15220.
 GN Name=DKFZp686P15220;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 GN NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RG The German Human cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BX640627; CAB5781.1; -.
 DR HSSP: P01861; 1ADQ.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_c1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF07654; Cl-set; 3.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 90.8%; Score 1258; DB 2; Length 472;
 Best Local Similarity 100.0%; Pred. No. 4.2e-90;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 241 EPKSCDKHTHTCPPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 300
 QY 61 NMVYDGVAVNNAKTKPREEQYNSTYRVVSVLTVTHQDWLNAGEYKCKVSNKALPAPIEKT 120
 DB 301 NMVYDGVAVNNAKTKPREEQYNSTYRVVSVLTVTHQDWLNAGEYKCKVSNKALPAPIEKT 360
 QY 121 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNNGQPENNYKTTP 180

Db 361 ISKAKQPREPQYTYLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTTP 420
 Qy 181 PVLDSGSPFLYSKLTVDKSRMOQGNVFCSCVWHEALHNHYTQKSLSLSPG 231
 Db 421 PVLDSGSPFLYSKLTVDKSRMOQGNVFCSCVWHEALHNHYTQKSLSLSPG 471

RESULT 10

ID 06GMW7 PRELIMINARY; PRT; 475 AA.
 AC 06GMW7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Matra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC073782; AAH73782.1; -
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG-cl.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF07654; Cl-sec; 3.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00409; Ig; 2.
 DR SMART: SM00407; IgC1; 3.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS50835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 475 AA; 51987 MW; 2A1PES5D7368608 CRC64;

Query Match 90.8%; Score 1258; DB 2; Length 475;
 Best Local Similarity 100.0%; Pred. No. 4.2e-90;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPRSCDKHTPCPCAPABELIGGDSVFLPPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
 Db 244 EPRSCDKHTPCPCAPABELIGGDSVFLPPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 303

Qy 61 NMYVDGEVHNAKTKPREEQYNSTYRVSVLTALHODMNLNGEKYCKCKVSKALPAPIEKT 120
 Db 304 NMYVDGEVHNAKTKPREEQYNSTYRVSVLTALHODMNLNGEKYCKCKVSKALPAPIEKT 363
 Qy 121 ISKAKQPREPQYTYLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTTP 180
 Db 364 ISKAKQPREPQYTYLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTTP 423

RESULT 11

ID 06GMX1 PRELIMINARY; PRT; 476 AA.
 AC 06GMX1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Matra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC073773; AAH73773.1; -
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG-cl.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF07654; Cl-sec; 3.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00409; Ig; 2.
 DR SMART: SM00407; IgC1; 3.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS50835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 476 AA; 52286 MW; 622AAB5C62DB9D CRC64;

Query Match 90.8%; Score 1258; DB 2; Length 476;
 Best Local Similarity 100.0%; Pred. No. 4.2e-90;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 245 EPKSCDKHTHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 304
 QY 61 NMVYDGEVHNKKTREBQVNSTYRVSVLTVLHQMVLNKEKYCKVSNKALPAPIEKT 120
 DB 305 NMVYDGEVHNKKTREBQVNSTYRVSVLTVLHQMVLNKEKYCKVSNKALPAPIEKT 364
 QY 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
 DB 365 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 424
 QY 181 PVLDSGSEFLYISKLTVDKSRMQGVNFCSCVMHEALHNHYTQKSLSISPG 231
 DB 425 PVLDSGSEFLYISKLTVDKSRMQGVNFCSCVMHEALHNHYTQKSLSISPG 475

RESULT 12

Q96P08 PRELIMINARY; PRT; 679 AA.
 AC Q96P08;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Factor VII active site mutant Immunocompugate.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxId=9606;
 RX MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
 RX Hu Z., Garen A.;
 RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
 RT cells for immunotherapy in mouse models of prostatic cancer.";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hu Z., Garen A.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF272774; AAK58686.2; -
 DR HSSP; P08709; IKLI.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004235; F:trypsin activity; IEA.
 DR GO; GO:000508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000152; Aex_Hydroxyl_5.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR000294; VitK_dep_Gla.
 DR Pfam; PF07654; Cl-sec; 2.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00020; TYP_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01166; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 KW EGF-like domain; Hydroxylase; Protease; Serine protease.
 KW EGF-like domain; Hydroxylase; Protease; Serine protease.
 SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;

Query Match 90.8%; Score 1258; DB 2; Length 679;
 Best Local Similarity 100.0%; Pred. No. 6; 6e-90;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 448 EPKSCDKHTHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 507
 QY 61 NMVYDGEVHNKKTREBQVNSTYRVSVLTVLHQMVLNKEKYCKVSNKALPAPIEKT 120
 DB 508 NMVYDGEVHNKKTREBQVNSTYRVSVLTVLHQMVLNKEKYCKVSNKALPAPIEKT 567
 QY 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
 DB 568 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 627
 QY 181 PVLDSGSEFLYISKLTVDKSRMQGVNFCSCVMHEALHNHYTQKSLSISPG 231
 DB 628 PVLDSGSEFLYISKLTVDKSRMQGVNFCSCVMHEALHNHYTQKSLSISPG 678

RESULT 13

Q6P055 PRELIMINARY; PRT; 473 AA.
 ID Q6P055;
 AC Q6P055;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxId=9606;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold B.A., Grouse L.H., Berger J.G.,
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Berger J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Matulis A.K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Stadelman M., Soares M.B., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Brownstein M.J., Ussid T.B., Toshiyuki S., Cantini P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Males J.A., Hulyk S.W.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Gay L.J., Hulyk S.W.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalobos D.K., Muzny D.M., Sodergren G.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smalins D.E., Schermer A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RA Strausberg R.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC065820; AA65820.1; -
 DR HSSP; P01861; IADO.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IgC1; 3.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51344 MW; 9816D56477129857 CRC64;

Query Match 90.5%; Score 1254; DB 2; Length 473;
 Best Local Similarity 99.6%; Pred. No. 8.7e-90;
 Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPKSCDKHTTCCPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 242 EPKSCDKHTTCCPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 301
 QY 61 NMYVDSGEVHNAAKTKRREQYNSTRVVSVLTVLHODMNGKRYCKKVSNNKALPAPIEKT 120
 DB 302 NMYVDSGEVHNAAKTKRREQYNSTRVVSVLTVLHODMNGKRYCKKVSNNKALPAPIEKT 361
 QY 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQEPENNYKTTTP 180
 DB 362 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQEPENNYKTTTP 421
 QY 181 PVLDSGSEFLYSKLTVDKSRWQGNVFCSVNHEALHNHYTQKSLSLSPG 231
 DB 422 PVLDSGSEFLYSKLTVDKSRWQGNVFCSVNHEALHNHYTQKSLSLSPG 472

RESULT 14

Q6MZ06 PRELIMINARY; PRT; 475 AA.
 AC 06MZ06;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686G11190.
 GN Name=DKFZp686G11190;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human esophagus tumor;
 RG The German Human CDNA Consortium;
 RA Lauber U., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
 RA Han M., Wiemann S.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640947; CAB45972.1; -.
 DR HSSP; P01861; IADO.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IgC1; 3.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 475 AA; 52043 MW; B7EAB255A26F4B8E CRC64;

Query Match 90.5%; Score 1254; DB 2; Length 475;
 Best Local Similarity 99.6%; Pred. No. 8.7e-90;
 Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPKSCDKHTTCCPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 244 EPKSCDKHTTCCPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
 QY 61 NMYVDSGEVHNAAKTKRREQYNSTRVVSVLTVLHODMNGKRYCKKVSNNKALPAPIEKT 120
 DB 304 NMYVDSGEVHNAAKTKRREQYNSTRVVSVLTVLHODMNGKRYCKKVSNNKALPAPIEKT 363
 QY 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQEPENNYKTTTP 180
 DB 364 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQEPENNYKTTTP 423

Query Match 90.5%; Score 1254; DB 2; Length 480;
 Best Local Similarity 99.6%; Pred. No. 8.8e-90;
 Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 181 PVLDSGSEFLYSKLTVDKSRWQGNVFCSVNHEALHNHYTQKSLSLSPG 231
 DB 424 PVLDSGSEFLYSKLTVDKSRWQGNVFCSVNHEALHNHYTQKSLSLSPG 474

RESULT 15

Q6N094 PRELIMINARY; PRT; 480 AA.
 AC 06N094;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686O01196.
 GN Name=DKFZp686O01196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human esophagus tumor;
 RG The German Human CDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640622; CAB45776.1; -.
 DR HSSP; P01861; IADO.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IgC1; 3.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 480 AA; 2252473D35AEC18 CRC64;

Query Match 90.5%; Score 1254; DB 2; Length 480;
 Best Local Similarity 99.6%; Pred. No. 8.8e-90;
 Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPKSCDKHTTCCPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 249 EPKSCDKHTTCCPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 308
 QY 61 NMYVDSGEVHNAAKTKRREQYNSTRVVSVLTVLHODMNGKRYCKKVSNNKALPAPIEKT 120
 DB 309 NMYVDSGEVHNAAKTKRREQYNSTRVVSVLTVLHODMNGKRYCKKVSNNKALPAPIEKT 368
 QY 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQEPENNYKTTTP 180
 DB 369 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQEPENNYKTTTP 428
 QY 181 PVLDSGSEFLYSKLTVDKSRWQGNVFCSVNHEALHNHYTQKSLSLSPG 231
 DB 429 PVLDSGSEFLYSKLTVDKSRWQGNVFCSVNHEALHNHYTQKSLSLSPG 479

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